RAW SEQUENCE LISTING DATE: 04/07/2003
PATENT APPLICATION: **US/09/720,383C** TIME: 08:02:21

Input Set : **N:\AMC\US09720383C.raw**
Output Set: **N:\CRF4\04072003\I720383C.raw**

ENTERED
p.6

1 <110> APPLICANT: Stephen M. Allen
2 Gary M. Fader
3 Saverio Carl Falco
4 Anthony J. Kinney
5 Jonathan E. Lightner
6 Guo-Hua Miao
7 J. Antoni Rafalski
8 Catherine J. Thorpe
9 <120> TITLE OF INVENTION: Plant Cellulose Synthases
10 <130> FILE REFERENCE: BB-1170
C--> 11 **<140> CURRENT APPLICATION NUMBER: US/09/720,383C**
12 <141> CURRENT FILING DATE: 2000-12-21
13 <150> PRIOR APPLICATION NUMBER: 60/092,844
14 <151> PRIOR FILING DATE: 1998-07-14
15 <160> NUMBER OF SEQ ID NOS: 29
16 <170> SOFTWARE: Microsoft Office 97
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1221
20 <212> TYPE: DNA
21 <213> ORGANISM: Hordeum vulgare
22 <400> SEQUENCE: 1
23 gcacgaggat attcttactg ggtttaaaat gcacgcaaga ggttggatat caatctactg 60
24 catgccacca cgaccttgtt tcaagggttc tgcgccaatc aatctctctg accgtctcaa 120
25 tcaagttctc cggtgggctc ttgggtcagt tgaaattctg tttagcagac attgtcctat 180
26 ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacaccat 240
27 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttcctg ctatctgtct 300
28 cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt tctttattct 360
29 tatgtttgcc tccatctttg ccacgggtat attggagctg cgatggagtg gtgtcggcat 420
30 cgaggactgg tggagaaacg agcagttctg ggttattggt ggcacatctg cccatctttt 480
31 cgcagtgttc cagggtctgc tgaaggtgtt ggccgggatt gacaccaact tcacggttac 540
32 ctcgaaggca aacgacgagg atggcgattt tgctgagtta tacgtgttca agtggaccag 600
33 tctcctcatt cctccgacca ccgtccttgt gattaacctg gtgggcatgg tggcaggcat 660
34 atcatatgcc atcaacagcg gttaccagtc ttggggtcca ctcttcggaa agctcttctt 720
35 ctcaatctgg gtgatcctcc atctctaccc cttcctcaag ggtctcatgg ggaagcagaa 780
36 ccgcacgcca accatcgtca ttgtttggtc catcctccta gcctccatct tctccctcct 840
37 gtgggtgaag atcgaccctt tcatatccga tacccagaaa gccgtcgcca tggggcagtg 900
38 tggcgtcaac tgctgatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg 960
39 gggttggatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc 1020
40 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat 1080
41 ttttttctcc ttttcttttc atctgtgata cctgttgttt cttcttagag tatattatgt 1140
42 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt 1200
43 tgcatcaact cttctgcaaa a 1221
45 <210> SEQ ID NO: 2

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Input Set : **N:\AMC\US09720383C.raw**
Output Set: **N:\CRF4\04072003\I720383C.raw**

<211> LENGTH: 304
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare
<400> SEQUENCE: 2

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His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
 1               5                  10                  15
Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro
            20                  25                  30
Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
        35                  40                  45
Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
    50                  55                  60
Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
65                  70                  75                  80
Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
                85                  90                  95
Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
            100                 105                 110
Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
        115                 120                 125
Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
    130                 135                 140
Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
145                 150                 155                 160
Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
                165                 170                 175
Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
            180                 185                 190
Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
        195                 200                 205
Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
    210                 215                 220
Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
225                 230                 235                 240
Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
                245                 250                 255
Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
            260                 265                 270
Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
        275                 280                 285
Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys
    290                 295                 300
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<210> SEQ ID NO: 3
<211> LENGTH: 3776
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<400> SEQUENCE: 3

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gcgcgccgcg caggcgcaac gcaacaaagg gaaaccccag ccggaggagc aaaagctagc   60
aagcgtgtcc ctccccctcc ctcactcccg tttcattcca ttccccccca gacgccgcta  120
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Input Set : **N:\AMC\US09720383C.raw**
Output Set: **N:\CRF4\04072003\I720383C.raw**

```
96    ccgccgccgc cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccaggggat  180
97    ggaggccagc gccgggctgg tcgccggctc gcacaaccgg aacgagctcg tcgtcatccg  240
98    ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat  300
99    ttgcggcgac gacgtggggc gcaaccccga cggggagccg ttcgtggcct gcaacgagtg  360
100    cgccttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaactg  420
101    cccccagtgc aagacccgct tcaagcgcct caaggggtgc gcgcgcgtgc ccggggacga  480
102    ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc  540
103    ccagtacctc gccgagtcca tgctccacgc ccacatgagc tacggccgcg gcgccgacct  600
104    cgacggcgtg ccgcagccat tccaccccat ccccaatgtt cccctcctca ccaacggaca  660
105    gatggtcgat gacatcccgc cggaccagca cgcccttgtg ccctcgttcg tgggtggcgg  720
106    ggggaagagg attcaccctc tcccgtacgc ggatcccaac cttcctgtgc aaccgaggtc  780
107    tatggaccct tccaaggatc tcgccgcata tggctacggg agcgtagcat ggaaggagag  840
108    gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaacg atggcggcgg  900
109    cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag  960
110    aaagatcccg cttccttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020
111    agtggttttg tgtttcttct tccactaccg agtgatgcat ccggtgcctg atgcatttgc 1080
112    tttatggctc atatctgtga tctgtgaaat ttggtttgcc atgtcttgga ttcttgacca 1140
113    gtttccaaag tggtttccta tcgagaggga aacctatctt gaccggctga gtttaaggtt 1200
114    tgacaaggaa gggcatcctt ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
115    tcccttgaag gaacctccat tggtcactgc taatactgtt ctatctatcc tttcggtgga 1320
116    ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
117    tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaagata 1440
118    tagccttgag cctcgtgctc cagagtggta cttccaacag aagatagact acctgaaaga 1500
119    caaggtggcg ccaaactttg ttagagaacg gagagcaatg aagagagagt atgaggaatt 1560
120    caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
121    aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680
122    ggttttcctt ggtcaaagtg gtggccatga tgtggaagga aatgagctgc ctcgattggt 1740
123    ttatgtttca agagaaaaac ggccaggcta caaccatcac aagaaggctg gtgctatgaa 1800
124    tgcattggtc cgagtctctg ctgtactaac taatgctcct tatttgctga acttggattg 1860
125    tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
126    tttgcttgga aagaaagttt gctatgtgca gtttcctcaa agatttgatg ggattgatcg 1980
127    ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aaggtttgga 2040
128    tggtatccag ggcccaattt atgtgggtac tggatgtgtc ttcagaaggc aggcattata 2100
129    tggctacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
130    gtggtgcatt tgctgttgct gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220
131    taaacctaaa tttgagaaga taaagaaact ttttaagaaa aaggaaaatc aagcccctgc 2280
132    atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340
133    tgtaaatcaa cagaagttgg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
134    acttcttgag aatggtggaa ccctgaagag tgccagtcca gcttctcttc tgaaggaagc 2460
135    tatacatgtc atcagttgtg gatatgaaga caaaacaggc tggggaaaag atattggttg 2520
136    gatttatgga tcagtcacag aagatattct tactgggttt aagatgcact gccatggttg 2580
137    gcggtcaatt tactgcatac ctaaacgggc cgccttcaaa ggttccgcac ctctcaatct 2640
138    ttccgatcgt cttcaccagg ttcttcggtg ggctcttggt tcaattgaaa ttttcttcag 2700
139    caaccactgc cctctctggt atgggtatgg tggtggacta aagttcctgg aaaggttttc 2760
140    gtacattaac tccatcgtat acccttggac atctatcccg ctcttggcct attgcacatt 2820
141    gcctgccatc tgcttgctga cagggaaatt tatcacgcca gagcttaaca atgttgccag 2880
142    cctctggttc atgtcacttt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940
143    gagtggtgta ggcatcgatg actggtggag aaacgagcag ttttgggtca ttggaggcgt 3000
144    gtcttcacat ctctttgctg tgttccaggg actcctcaag gtcatagctg gtgtagacac 3060
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gagcttcact gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120
caaatggacg acccttctga tacctccgac aaccctgctc ctactgaact tcattggagt 3180
ggtagctggc atctccaatg cgatcaacaa cggatatgaa tcatggggcc ccctgttcgg 3240
gaagctcttc tttgcatttt gggtgatcgt ccatctttac ccgttcctca agggtctggt 3300
tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
tggtcgaaga agtatttttg cagatgtttt gtgcccatat ttctttttc aatttttgtc 3540
cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600
atggtggtgg tggtggtggg cggctcagcc tcgtgagtgc agtattgggc aaaccggagg 3660
ctgcggcaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776

<210> SEQ ID NO: 4
<211> LENGTH: 1148
<212> TYPE: PRT
<213> ORGANISM: Zea mays
<400> SEQUENCE: 4

Arg Ala Ala Gln Ala Gln Arg Asn Lys Gly Lys Pro Gln Pro Glu Glu
1 5 10 15
Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
20 25 30
Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
35 40 45
Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
50 55 60
Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
65 70 75 80
Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
85 90 95
Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
100 105 110
Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
115 120 125
Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
130 135 140
Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
145 150 155 160
Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
165 170 175
Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
180 185 190
Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
195 200 205
Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
210 215 220
Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
225 230 235 240
Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
245 250 255

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Input Set : N:\AMC\US09720383C.raw
Output Set: N:\CRF4\04072003\I720383C.raw

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195  Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
196                  260                 265                 270
197  Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
198              275                 280                 285
199  Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
200          290                 295                 300
201  Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
202  305                 310                 315                 320
203  Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
204                      325                 330                 335
205  Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
206                  340                 345                 350
207  His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
208              355                 360                 365
209  Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
210          370                 375                 380
211  Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
212  385                 390                 395                 400
213  Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
214                      405                 410                 415
215  Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
216                  420                 425                 430
217  Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
218              435                 440                 445
219  Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
220          450                 455                 460
221  Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
222  465                 470                 475                 480
223  Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
224                      485                 490                 495
225  Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
226                  500                 505                 510
227  Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
228              515                 520                 525
229  Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
230          530                 535                 540
231  Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
232  545                 550                 555                 560
233  Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
234                      565                 570                 575
235  Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
236                  580                 585                 590
237  His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
238              595                 600                 605
239  Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
240          610                 615                 620
241  Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
242  625                 630                 635                 640
243  Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/07/2003
PATENT APPLICATION: **US/09/720,383C** TIME: 08:02:22

Input Set : **N:\AMC\US09720383C.raw**
Output Set: **N:\CRF4\04072003\I720383C.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 201
Seq#:19; N Pos. 262
Seq#:20; Xaa Pos. 88